

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising a nucleotide sequence:
 - (a) as set forth in SEQ ID NO: 1;
 - 5 (b) encoding a polypeptide as set forth in SEQ ID NO: 2; or
 - (c) that is complementary to the nucleotide sequence of either (a) or (b).

2. An isolated nucleic acid molecule comprising a nucleotide sequence:
 - (a) as set forth in SEQ ID NO: 1;
 - 10 (b) encoding a polypeptide as set forth in SEQ ID NO: 2;
 - (c) that hybridizes to the complement of the nucleotide sequence of either (a) or (b) under hybridization conditions allowing no more than a 21% mismatch between the nucleotide sequences; or
 - (d) that is complementary to the nucleotide sequence of any of (a) - (c).

- 15 3. An isolated nucleic acid molecule comprising:
 - (a) a region of the nucleotide sequence of SEQ ID NO: 1 encoding a polypeptide fragment of at least 25 amino acid residues;
 - (b) a region of the nucleotide sequence of SEQ ID NO: 1 comprising a
20 fragment of at least 16 nucleotides;
 - (c) a nucleotide sequence that hybridizes to the complement of the nucleotide sequence of either (a) or (b) under hybridization conditions allowing no more than a 21% mismatch between the nucleotide sequences; or
 - 25 (d) a nucleotide sequence that is complementary to the nucleotide sequence of any of (a) - (c).

4. An isolated nucleic acid molecule comprising:

- (a) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one conservative amino acid substitution, wherein the encoded polypeptide is at least 70 percent identical to the polypeptide set forth in SEQ ID NO: 2;
- 5 (b) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 having a C- and/or N- terminal truncation, wherein the encoded polypeptide comprises at least 25 amino acid residues;
- (c) a nucleotide sequence encoding a polypeptide as set forth in SEQ ID NO: 2 with at least one modification that is a conservative amino acid substitution, C-terminal truncation, or N-terminal truncation, wherein
10 the encoded polypeptide is at least 70 percent identical to the polypeptide set forth in SEQ ID NO: 2 and comprises at least 25 amino acid residues;
- (d) a region of the nucleotide sequence of any of (a) - (c) comprising a
15 fragment of at least 16 nucleotides;
- (e) a nucleotide sequence that hybridizes to the complement of the nucleotide sequence of any one of (a) - (d) under hybridization conditions allowing no more than a 21% mismatch between the nucleotide sequences; or
- 20 (f) a nucleotide sequence that is complementary to the nucleotide sequence of any of (a) - (e).

- 5. A vector comprising the nucleic acid molecule of any of Claims 1, 2, 3, or 4.
- 25 6. A host cell comprising the vector of Claim 5.
- 7. The host cell of Claim 6 that is a eukaryotic cell.
- 8. The host cell of Claim 6 that is a prokaryotic cell.

9. A process of producing an IL-1ra-L polypeptide comprising culturing the host cell of Claim 6 under suitable conditions to express the polypeptide, and optionally isolating the polypeptide from the culture.

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10. The process of Claim 9, wherein the nucleic acid molecule comprises promoter DNA other than native IL-1ra-L promoter DNA operatively linked to a nucleic acid molecule encoding an IL-1ra-L polypeptide.

10 11. The isolated nucleic acid molecule according to Claim 4, wherein the percent identity is determined using a computer program that is GAP, BLASTN, FASTA, BLASTA, BLASTX, BestFit, or the Smith-Waterman algorithm.

12. A composition comprising a nucleic acid molecule of any of Claims 1, 2, 3, or 4
15 and a pharmaceutically acceptable formulation agent.

13. The composition of Claim 12, wherein said nucleic acid molecule is contained in a viral vector.

20 14. A viral vector comprising a nucleic acid molecule of any of Claims 1, 2, 3, or 4.

15. A nucleic acid molecule encoding a fusion polypeptide comprising the nucleic acid molecule of any of Claims 1, 2, 3, or 4 fused to DNA encoding a heterologous amino acid sequence.

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16. The nucleic acid molecule of Claim 15, wherein the DNA encoding the heterologous amino acid sequence encodes an IgG constant domain or biologically active fragment thereof.